SEQUENCE LISTING

<110> ITO, Kikukatsu

<120> Plant Thermogenic Genes and Proteins

<130> 2001-1838A/LC/00653

<140> 10/009,962
<141> 2002-01-23

<150> PCT/JP00/03806
<151> 2000-06-12

<150> JP11-167439
<151> 1999-06-14

<160> 12

<170> PatentIn Ver. 2.0

<210> 1
<211> 1525
<212> DNA
<213> Symplocarpus foetidus

<220>
<221> CDS
<222> (280)..(1188)
<221> poly A site
<221> (1271)..(1276)

<300>
<301> Ito, K.
<302> Isolation of two distinct cold-inducible cDNAs encoding plant uncoupling p
roteins from the
spadix of skunk cabbage (Symplocarpus foetidus)
<303> Plant Sci.
<304> 149
<305> 2
<306> 167-173
<307> Dec-1999
<308> GenBank AB024733
<309> 2000-02-25

<400> 1
gaggattcgc agaagaaagg ccagaacccg attccttccc gtcttcttct ccttccgccc 60
aattgcagtt tttcgcagcg gcgtcatcat caagaccctc cgcctttccg cgccaaacgc 120
cttccacccc cacccaatcg ccctccgttt cccgaaatat tcctcttccc tcctcccttt 180
tcttctctac ataaacccta accaccccat cctctcctcc cgcttccgac caccctgcat 240
tctactggga gcccatttga tcgaggtttc ccggcgagg atg ggc gat cac ggc 294
Met Gly Asp His Gly
1 5
ccg agg acc gag atc tcg ttt gcc ggc agt tcg cga gca gca ttc gcc 342
Pro Arg Thr Glu Ile Ser Phe Ala Gly Ser Ser Arg Ala Ala Phe Ala
10 15 20
gct tgc ttc gcc gag ctt tgc acg att ccg ttg gac act gct aaa gtt 390

```
Ala Cys Phe Ala Glu Leu Cys Thr Ile Pro Leu Asp Thr Ala Lys Val
                25                  30                  35
agg ctt caa ctc caa aag aaa gca gta aca ggt gat gtg gtg gct ttg   438
Arg Leu Gln Leu Gln Lys Lys Ala Val Thr Gly Asp Val Val Ala Leu
            40                  45                  50
cca aaa tac agg gga atg ttg ggc act gtt gcc act att gcc agg gag   486
Pro Lys Tyr Arg Gly Met Leu Gly Thr Val Ala Thr Ile Ala Arg Glu
        55                  60                  65
gaa ggt ttg tcg gca ctc tgg aaa gga att gta ccc ggt ttg cat cgt   534
Glu Gly Leu Ser Ala Leu Trp Lys Gly Ile Val Pro Gly Leu His Arg
    70                  75                  80                  85
caa tgc ctc ttt gga ggg cta cga att ggg ttg tat gaa cca gtt aag   582
Gln Cys Leu Phe Gly Gly Leu Arg Ile Gly Leu Tyr Glu Pro Val Lys
                90                  95                  100
tcc ttt tat gtt gga gat aac ttt gtt gga gat att cct tta tcc aag   630
Ser Phe Tyr Val Gly Asp Asn Phe Val Gly Asp Ile Pro Leu Ser Lys
            105                 110                 115
aaa ata ctt gct ggg ctt aca aca ggt gca tta gca att ata gtg gca   678
Lys Ile Leu Ala Gly Leu Thr Thr Gly Ala Leu Ala Ile Ile Val Ala
        120                 125                 130
aat ccc act gac ctt gtt aaa gtt cga ctt caa tct gaa ggt aaa ctc   726
Asn Pro Thr Asp Leu Val Lys Val Arg Leu Gln Ser Glu Gly Lys Leu
    135                 140                 145
ccc cct ggg gta ccg aga cgt tat tca ggg gcg cta aat gct tat tca   774
Pro Pro Gly Val Pro Arg Arg Tyr Ser Gly Ala Leu Asn Ala Tyr Ser
150                 155                 160                 165
acc ata gtc aaa aag gaa gga ctt ggt gct ctg tgg act ggg ctt ggt   822
Thr Ile Val Lys Lys Glu Gly Leu Gly Ala Leu Trp Thr Gly Leu Gly
                170                 175                 180
cct aat att gcc cgc aat gct att ata aat gct gct gaa ttg gcc agt   870
Pro Asn Ile Ala Arg Asn Ala Ile Ile Asn Ala Ala Glu Leu Ala Ser
            185                 190                 195
tat gat caa gtg aaa cag aca atc tta aaa tta cca gga ttc tca gat   918
Tyr Asp Gln Val Lys Gln Thr Ile Leu Lys Leu Pro Gly Phe Ser Asp
        200                 205                 210
aat att ttt act cat att tta gcc ggt ctg ggg gca ggt ttt ttt gcc   966
Asn Ile Phe Thr His Ile Leu Ala Gly Leu Gly Ala Gly Phe Phe Ala
    215                 220                 225
gtc tgt atc ggt tct cct gtt gat gtg atg aag tct aga atg atg gga   1014
Val Cys Ile Gly Ser Pro Val Asp Val Met Lys Ser Arg Met Met Gly
230                 235                 240                 245
gat tca gcc tac aaa agc aca ttt gat tgt ttc atc aag aca ttg aaa   1062
Asp Ser Ala Tyr Lys Ser Thr Phe Asp Cys Phe Ile Lys Thr Leu Lys
                250                 255                 260
aat gat ggg ctt ctt gct ttt tac aag ggg ttt atc cca aac ttt ggt   1110
Asn Asp Gly Leu Leu Ala Phe Tyr Lys Gly Phe Ile Pro Asn Phe Gly
            265                 270                 275
cgg tta gga tcg tgg aat gtg atc atg ttt ttg acc ttg gag cag gtc   1158
Arg Leu Gly Ser Trp Asn Val Ile Met Phe Leu Thr Leu Glu Gln Val
        280                 285                 290
aag aag ttt ttc atc aaa gag gtg cca aat taatacattg aactcggata     1208
Lys Lys Phe Phe Ile Lys Glu Val Pro Asn
    295                 300
ggagtagaaa gaaagggttt ttgtggaatt ttctctaccg gtgtggatcc tggcgagaga 1268
caaataaatc ttcctgactg ctcagatgtg taccttttt atgaatggtt cttttcttat 1328
agaggacaga gaaaagaaaa aaaaaatcat tgtcatttac tctttttccc catttctgct 1388
gctaatcttg gtaggagaag aaaagtctta cattgagtga taacgttgtt ctctgcatcc 1448
```

attatttttc agagatacta tttgacacat gaaaagtaat gcacatcagg ttttttttaa 1508
aaaaaaaaaa aaaaaaa 1525

<210> 2
<211> 303
<212> PRT
<213> Symplocarpus foetidus

<400> 2
Met Gly Asp His Gly Pro Arg Thr Glu Ile Ser Phe Ala Gly Ser Ser
1 5 10 15
Arg Ala Ala Phe Ala Ala Cys Phe Ala Glu Leu Cys Thr Ile Pro Leu
20 25 30
Asp Thr Ala Lys Val Arg Leu Gln Leu Gln Lys Lys Ala Val Thr Gly
35 40 45
Asp Val Val Ala Leu Pro Lys Tyr Arg Gly Met Leu Gly Thr Val Ala
50 55 60
Thr Ile Ala Arg Glu Glu Gly Leu Ser Ala Leu Trp Lys Gly Ile Val
65 70 75 80
Pro Gly Leu His Arg Gln Cys Leu Phe Gly Gly Leu Arg Ile Gly Leu
85 90 95
Tyr Glu Pro Val Lys Ser Phe Tyr Val Gly Asp Asn Phe Val Gly Asp
100 105 110
Ile Pro Leu Ser Lys Lys Ile Leu Ala Gly Leu Thr Thr Gly Ala Leu
115 120 125
Ala Ile Ile Val Ala Asn Pro Thr Asp Leu Val Lys Val Arg Leu Gln
130 135 140
Ser Glu Gly Lys Leu Pro Pro Gly Val Pro Arg Arg Tyr Ser Gly Ala
145 150 155 160
Leu Asn Ala Tyr Ser Thr Ile Val Lys Lys Glu Gly Leu Gly Ala Leu
165 170 175
Trp Thr Gly Leu Gly Pro Asn Ile Ala Arg Asn Ala Ile Ile Asn Ala
180 185 190
Ala Glu Leu Ala Ser Tyr Asp Gln Val Lys Gln Thr Ile Leu Lys Leu
195 200 205
Pro Gly Phe Ser Asp Asn Ile Phe Thr His Ile Leu Ala Gly Leu Gly
210 215 220
Ala Gly Phe Phe Ala Val Cys Ile Gly Ser Pro Val Asp Val Met Lys
225 230 235 240
Ser Arg Met Met Gly Asp Ser Ala Tyr Lys Ser Thr Phe Asp Cys Phe
245 250 255
Ile Lys Thr Leu Lys Asn Asp Gly Leu Leu Ala Phe Tyr Lys Gly Phe
260 265 270
Ile Pro Asn Phe Gly Arg Leu Gly Ser Trp Asn Val Ile Met Phe Leu
275 280 285
Thr Leu Glu Gln Val Lys Lys Phe Phe Ile Lys Glu Val Pro Asn
290 295 300

<210> 3
<211> 2991
<212> DNA
<213> Symplocarpus foetidus

<220>
<221> CDS
<222> (286)..(1089)
<221> poly A site

<222> (1171)..(1176)
<221> poly A site
<222> (1243)..(1248)

<300>
<301> Ito, K.
<302> Isolation of two distinct cold-inducible cDNAs encoding plant uncoupling p
roteins from the
spadix of skunk cabbage (Symplocarpus foetidus)
<303> Plant Sci.
<304> 149
<305> 2
<306> 167-173
<307> Dec-1999
<308> GenBank AB024734
<309> 2000-02-25

<400> 3
tggtggtgac gagtgacgag gattcgcaga agaaaggcca gaacccgatt ccttcccgtc 60
ttcttctcct tccgcccaat tgcagttttt cgcagcgggt catcatcaag accctccgcc 120
tttccgcgcc aaacgccttc cacccaatcc ctccgtttcc cgaaatattc cccttccctc 180
ccttttcttc tctacataaa ccctaaccac ccccatcctc tcctcccgct tccgaccacc 240
ctgcattcta ctgggatccc atttgatcga cgtttcccgg cgagg atg ggc gat cac 297
                                                Met Gly Asp His
                                                  1
ggc ccg agg acc gag atc tcg ttt gcc ggc agt tcg cga gca gca ttc 345
Gly Pro Arg Thr Glu Ile Ser Phe Ala Gly Ser Ser Arg Ala Ala Phe
  5   10   15   20
gcc gct tgc ttc gcc gag ctc tgt acg att ccg ttg gac act gct aaa 393
Ala Ala Cys Phe Ala Glu Leu Cys Thr Ile Pro Leu Asp Thr Ala Lys
                 25   30   35
gtt agg ctt cag ctc caa aag aaa gca gta aca ggt gat gtg gtg gct 441
Val Arg Leu Gln Leu Gln Lys Lys Ala Val Thr Gly Asp Val Val Ala
             40   45   50
ttg cca aaa tac agg gga atg ttg ggc act gtt gcc act att gcc agg 489
Leu Pro Lys Tyr Arg Gly Met Leu Gly Thr Val Ala Thr Ile Ala Arg
         55   60   65
gag gaa ggt ttg tcg gca ctc tgg aaa gga att gta ccc ggt ttg cat 537
Glu Glu Gly Leu Ser Ala Leu Trp Lys Gly Ile Val Pro Gly Leu His
     70   75   80
cgt caa tgc ctc ttt gga ggg cta cga att ggg ttg tat gaa cca gtt 585
Arg Gln Cys Leu Phe Gly Gly Leu Arg Ile Gly Leu Tyr Glu Pro Val
 85   90   95   100
aag tcc ttt tat gtt gga gat aac ttt gtt gga gat att cct tta tcc 633
Lys Ser Phe Tyr Val Gly Asp Asn Phe Val Gly Asp Ile Pro Leu Ser
                105   110   115
aag aaa ata ctt gct ggg ctt aca aca ggt gca tta gca att ata gtg 681
Lys Lys Ile Leu Ala Gly Leu Thr Thr Gly Ala Leu Ala Ile Ile Val
            120   125   130
gca aat ccg act gac ctt gtt aaa gtt cga ctt caa tct gaa ggt aaa 729
Ala Asn Pro Thr Asp Leu Val Lys Val Arg Leu Gln Ser Glu Gly Lys
        135   140   145
ctc ccc cct ggg gta cca aga cgt tat tca ggg gcg cta aat gct tat 777
Leu Pro Pro Gly Val Pro Arg Arg Tyr Ser Gly Ala Leu Asn Ala Tyr
    150   155   160
tca acc ata gtc aaa aag gaa gga ctt ggt gct ctg tgg act ggg ctt 825
Ser Thr Ile Val Lys Lys Glu Gly Leu Gly Ala Leu Trp Thr Gly Leu

```
165                 170                 175                 180
ggt cct aat att gcc cgc aat gct att ata aat gct gct gaa ttg gcc   873
Gly Pro Asn Ile Ala Arg Asn Ala Ile Ile Asn Ala Ala Glu Leu Ala
                185                 190                 195
agt tat gat caa gtg aaa cag atg aag tct aga atg atg gga gat tca   921
Ser Tyr Asp Gln Val Lys Gln Met Lys Ser Arg Met Met Gly Asp Ser
            200                 205                 210
gcc tac aaa agc aca ttt gat tgt ttc atc aag acg ttg aaa aat gat   969
Ala Tyr Lys Ser Thr Phe Asp Cys Phe Ile Lys Thr Leu Lys Asn Asp
        215                 220                 225
ggg cct ctt gct ttt tac aag ggg ttt atc cca aac ttt ggt cgg tta   1017
Gly Pro Leu Ala Phe Tyr Lys Gly Phe Ile Pro Asn Phe Gly Arg Leu
    230                 235                 240
gga tcg tgg aat gtg atc atg ttt ttg acc ttg gag cag gtc aag aag   1065
Gly Ser Trp Asn Val Ile Met Phe Leu Thr Leu Glu Gln Val Lys Lys
245                 250                 255                 260
ttc ttc atc aaa gag gtg cca aat taatacattg aagtcggata ggagtagaaa  1119
Phe Phe Ile Lys Glu Val Pro Asn
                265
aaaagggttt ttgtggaatt ttctctaccg gtgtggatcc tggcgagaga gaataaatct 1179
tcctgactgc tcagatgttg tacctttttt atgaatggtt cttttcttat agaggacaga 1239
gaaaataaaa gaaaaattca ttgtcatgta ctctttttcc ccatttctgc tgagtagcag 1299
ctataccaag cagactttgt tgcttggctg ctgctaatct tgtagctgaa gaaaagtctt 1359
acattgagtg ataacgttgt tctctgcatc cattattttt cagagttact atttgacaca 1419
tgaaaagttt ttttttttt ttttttttt aacaggcagc aaatagagga atcgatctca 1479
cgactatcct ctttattcat taacaggcat acaaacttag ggagagcatg cagggtatat 1539
atcaaaatat acccttttat tagacatttt gcgtacacag ttggtcctca aacgactgta 1599
tctagcagcc aatttttaga ccacattaag acagagagaa acaagcagaa gaacagggta 1659
ccatacatac ataggtaata attaagatga tgaacatagc ataggttcat gatctacttc 1719
ttcttcacgt acacatgatg caccagctga atgggaatct tggtcaccat atggcatgaa 1779
agtacgtcat gtgcagacgt tatatagtgt tcttcttacc attcagcagc agcaccagag 1839
gcatcaaaca ctggggtctt gacagggtat gaggggtaca ttgcgatccc acacatgccg 1899
tagggagtca cattgcgttt gatttttatg tatccagcct gtccccacct agtgccccat 1959
gagttcctta caagccaata atccttccca tcctccgaac catatcctat tatcaccaca 2019
gcatggtcga tacgttgacc acatggtcca gcaaatacgc ccgaggtgta gtgttggaat 2079
ccagcgcccg aagcctcaag agcaacactg acaggttgct ttgcgactgc atactgtagg 2139
ctaacctcgt tgtacggaga aacattttca tacgcatcaa tcgaggtgac tttaataaga 2199
tttgctctgc aagttcctcg acgtcctgtg tacgggtaat ttttgaaaaa aggagaaggg 2259
cgggaagaag cgcgcgtctc tgctcgcgac gggttaattc ttcatatggc cacttcgagc 2319
atggcttcgg cagcctccag cttcgttctc actccggcct cccctccacc accacgccgg 2379
ttcccccgtc cgccttcttt cccagggtcg caggaggctc gtggtggtgc gggccgagga 2439
agccgcgacg acccccgccc ccggcgccgg cggagggagc cgcgccgccg cccccaagcc 2499
gccaccgatc gggcccaaga gggggtcaaa ggttgatata tagttcttaa tttctttccc 2559
gtgtggcttc tggagttaga tttgtttcct cttctctttt tttgttttgt tttttcaatt 2619
taaattttat tctcatctgt ggacgacctt ccatcggggt tttcgtccct ctcgcaggtg 2679
aagatctccg gaaggaatcc tactggttca acggtgtcgg atcggtggtg gctgttgatc 2739
aggatccggc gactcgatac ccggtcgtgg ttcggttcac caaggtcaac tatgcgaacg 2799
tctcgaccaa caactacgca ctggacgaga tcctggaggt gaaatgaggg tcggcgggcg 2859
tggtcggtcg ggcatgtcac gatgatgtat tttcgcagtt ggtagtgtaa aataccatgt 2919
cattcgtgta aaactctttc gttcgccaaa tcctcagttg aaattttaat tcccagccag 2979
taaaaaaaaa aa                                                    2991
```

<210> 4
<211> 268
<212> PRT
<213> Symplocarpus foetidus

<400> 4
Met Gly Asp His Gly Pro Arg Thr Glu Ile Ser Phe Ala Gly Ser Ser
1 5 10 15
Arg Ala Ala Phe Ala Ala Cys Phe Ala Glu Leu Cys Thr Ile Pro Leu
20 25 30
Asp Thr Ala Lys Val Arg Leu Gln Leu Gln Lys Lys Ala Val Thr Gly
35 40 45
Asp Val Val Ala Leu Pro Lys Tyr Arg Gly Met Leu Gly Thr Val Ala
50 55 60
Thr Ile Ala Arg Glu Glu Gly Leu Ser Ala Leu Trp Lys Gly Ile Val
65 70 75 80
Pro Gly Leu His Arg Gln Cys Leu Phe Gly Gly Leu Arg Ile Gly Leu
85 90 95
Tyr Glu Pro Val Lys Ser Phe Tyr Val Gly Asp Asn Phe Val Gly Asp
100 105 110
Ile Pro Leu Ser Lys Lys Ile Leu Ala Gly Leu Thr Thr Gly Ala Leu
115 120 125
Ala Ile Ile Val Ala Asn Pro Thr Asp Leu Val Lys Val Arg Leu Gln
130 135 140
Ser Glu Gly Lys Leu Pro Pro Gly Val Pro Arg Arg Tyr Ser Gly Ala
145 150 155 160
Leu Asn Ala Tyr Ser Thr Ile Val Lys Lys Glu Gly Leu Gly Ala Leu
165 170 175
Trp Thr Gly Leu Gly Pro Asn Ile Ala Arg Asn Ala Ile Ile Asn Ala
180 185 190
Ala Glu Leu Ala Ser Tyr Asp Gln Val Lys Gln Met Lys Ser Arg Met
195 200 205
Met Gly Asp Ser Ala Tyr Lys Ser Thr Phe Asp Cys Phe Ile Lys Thr
210 215 220
Leu Lys Asn Asp Gly Pro Leu Ala Phe Tyr Lys Gly Phe Ile Pro Asn
225 230 235 240
Phe Gly Arg Leu Gly Ser Trp Asn Val Ile Met Phe Leu Thr Leu Glu
245 250 255
Gln Val Lys Lys Phe Phe Ile Lys Glu Val Pro Asn
260 265

<210> 5
<211> 306
<212> PRT
<213> Solanum Tuberosum

<400> 5
Met Gly Gly Gly Asp His Gly Gly Lys Ser Asp Ile Ser Phe Ala Gly
1 5 10 15

Ile Phe Ala Ser Ser Ala Phe Ala Ala Cys Phe Ala Glu Ala Cys Thr
20 25 30

Leu Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Leu Gln Lys Lys Ala
35 40 45

Val Glu Gly Asp Gly Leu Ala Leu Pro Lys Tyr Arg Gly Leu Leu Gly
50 55 60

Thr Val Gly Thr Ile Ala Lys Glu Glu Gly Ile Ala Ser Leu Trp Lys
65 70 75 80

```
Gly Ile Val Pro Gly Leu His Arg Gln Cys Ile Tyr Gly Gly Leu Arg
                 85                  90                  95

Ile Gly Met Tyr Glu Pro Val Lys Asn Leu Tyr Val Gly Lys Asp His
            100                 105                 110

Val Gly Asp Val Pro Leu Ser Lys Lys Ile Leu Ala Ala Leu Thr Thr
        115                 120                 125

Gly Ala Leu Gly Ile Thr Ile Ala Asn Pro Thr Asp Leu Val Lys Val
    130                 135                 140

Arg Leu Gln Ala Glu Gly Lys Leu Pro Ala Gly Val Pro Arg Arg Tyr
145                 150                 155                 160

Ser Gly Ala Leu Asn Ala Tyr Ser Thr Ile Val Lys Gln Glu Gly Val
                165                 170                 175

Arg Ala Leu Trp Thr Gly Leu Gly Pro Asn Ile Gly Arg Asn Ala Ile
            180                 185                 190

Ile Asn Ala Ala Glu Leu Ala Ser Tyr Asp Gln Val Lys Glu Ala Val
        195                 200                 205

Leu Arg Ile Pro Gly Phe Thr Asp Asn Val Val Thr His Leu Ile Ala
    210                 215                 220

Gly Leu Gly Ala Gly Phe Phe Ala Val Cys Ile Gly Ser Pro Val Asp
225                 230                 235                 240

Val Val Lys Ser Arg Met Met Gly Asp Ser Ala Tyr Lys Asn Thr Leu
                245                 250                 255

Asp Cys Phe Val Lys Thr Leu Lys Asn Asp Gly Pro Leu Ala Phe Tyr
            260                 265                 270

Lys Gly Phe Ile Pro Asn Phe Gly Arg Leu Gly Ser Trp Asn Val Ile
        275                 280                 285

Met Phe Leu Thr Leu Glu Gln Ala Lys Lys Phe Val Lys Ser Leu Glu
    290                 295                 300

Ser Pro
305
```

<210> 6
<211> 316
<212> PRT
<213> Arabidopsis thaliana

<400> 6

```
Met Val Ala Ala Gly Lys Ser Asp Leu Ser Leu Pro Lys Thr Phe Ala
  1               5                  10                  15

Cys Ser Ala Phe Ala Ala Cys Val Gly Glu Val Cys Thr Ile Pro Leu
             20                  25                  30
```

```
Asp Thr Ala Lys Val Arg Leu Gln Leu Gln Lys Ser Ala Phe Thr Leu
         35                  40                  45

Ala Gly Asp Val Thr Leu Pro Lys Tyr Arg Gly Leu Leu Gly Thr Val
     50                  55                  60

Gly Thr Ile Ala Arg Glu Glu Gly Leu Arg Ser Leu Trp Lys Gly Val
 65                  70                  75                  80

Val Pro Gly Leu His Arg Gln Cys Leu Phe Gly Gly Leu Arg Ile Gly
                 85                  90                  95

Met Tyr Glu Pro Val Lys Asn Leu Tyr Val Phe Thr Gly Lys Asp Phe
            100                 105                 110

Val Gly Asp Val Pro Leu Ser Lys Lys Ile Leu Ala Gly Leu Thr Thr
        115                 120                 125

Gly Ala Leu Gly Ile Met Val Ala Asn Pro Thr Asp Leu Val Lys Val
    130                 135                 140

Arg Leu Gln Ala Glu Gly Lys Leu Ala Ala Gly Ala Pro Arg Arg Tyr
145                 150                 155                 160

Ser Gly Ala Leu Asn Ala Tyr Phe Thr Ser Thr Ile Val Arg Gln Glu
                165                 170                 175

Gly Val Arg Ala Leu Trp Thr Val Leu Gly Pro Asn Val Ala Arg Asn
            180                 185                 190

Ala Ile Ile Asn Ala Ala Glu Leu Ala Ser Tyr Asp Gln Val Lys Glu
        195                 200                 205

Thr Ile Leu Lys Ile Pro Gly Phe Thr Asp Asn Val Val Thr His Ile
    210                 215                 220

Leu Ser Gly Leu Phe Thr Gly Ala Gly Phe Phe Ala Val Cys Ile Gly
225                 230                 235                 240

Ser Pro Val Asp Val Val Lys Ser Arg Met Met Gly Asp Ser Gly Ala
                245                 250                 255

Tyr Lys Gly Thr Ile Asp Cys Phe Val Lys Thr Leu Lys Ser Asp Gly
            260                 265                 270

Pro Met Ala Phe Tyr Lys Gly Phe Ile Pro Asn Phe Gly Arg Leu Gly
        275                 280                 285

Ser Phe Thr Trp Asn Val Ile Met Phe Leu Thr Leu Glu Gln Ala Lys
    290                 295                 300

Lys Tyr Val Arg Glu Leu Asp Ala Ser Lys Arg Asn
305                 310                 315
```

<210> 7
<211> 307

<212> PRT
<213> Homo sapiens

<400> 7

```
Met Gly Gly Leu Thr Ala Ser Asp Val His Pro Thr Leu Gly Val Gln
  1               5                  10                  15

Leu Phe Ser Ala Pro Ile Ala Ala Cys Leu Ala Asp Val Ile Thr Phe
            20                  25                  30

Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Val Gln Gly Glu Cys Pro
        35                  40                  45

Thr Ser Ser Val Ile Arg Tyr Lys Gly Val Leu Gly Thr Ile Thr Ala
    50                  55                  60

Val Val Lys Thr Glu Gly Arg Met Lys Leu Tyr Ser Gly Leu Pro Ala
65                  70                  75                  80

Gly Leu Gln Arg Gln Ile Ser Ser Ala Ser Leu Arg Ile Gly Leu Tyr
                85                  90                  95

Asp Thr Val Gln Glu Phe Leu Thr Ala Gly Lys Glu Thr Ala Pro Ser
            100                 105                 110

Leu Gly Ser Lys Ile Leu Ala Gly Leu Thr Thr Gly Gly Val Ala Val
        115                 120                 125

Phe Ile Gly Gln Pro Thr Glu Val Val Lys Val Arg Leu Gln Ala Gln
    130                 135                 140

Ser His Leu His Gly Ile Lys Pro Arg Tyr Thr Gly Thr Tyr Asn Ala
145                 150                 155                 160

Tyr Arg Ile Ile Ala Thr Thr Glu Gly Leu Thr Gly Leu Trp Lys Gly
                165                 170                 175

Thr Thr Pro Asn Leu Met Arg Ser Val Ile Ile Asn Cys Thr Glu Leu
            180                 185                 190

Val Thr Tyr Asp Leu Met Lys Glu Ala Phe Val Lys Asn Asn Ile Leu
        195                 200                 205

Ala Asp Asp Val Pro Cys His Leu Val Ser Ala Leu Ile Ala Gly Phe
    210                 215                 220

Cys Ala Thr Ala Met Ser Ser Pro Val Asp Val Val Lys Thr Arg His
225                 230                 235                 240

Ile Asn Ser Pro Pro Gly Gln Tyr Lys Ser Val Pro Asn Cys Ala Met
                245                 250                 255

Lys Val Phe Thr Asn Glu Gly Pro Thr Ala Phe Phe Lys Gly Leu Val
            260                 265                 270

Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Ile Met Phe Val Cys
        275                 280                 285
```

```
Phe Glu Gln Leu Lys Arg Glu Leu Ser Lys Ser Arg Gln Thr Met Asp
    290                 295                 300

Cys Ala Thr
305
```

<210> 8
<211> 309
<212> PRT
<213> Homo sapiens

<400> 8

```
Met Val Gly Phe Lys Ala Thr Asp Val Pro Pro Thr Ala Thr Val Lys
  1               5                  10                  15

Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala Asp Leu Ile Thr Phe
             20                  25                  30

Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln
         35                  40                  45

Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr Arg Gly Val Met Gly
     50                  55                  60

Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn
 65                  70                  75                  80

Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg
                 85                  90                  95

Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu
            100                 105                 110

His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala
        115                 120                 125

Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
    130                 135                 140

Gln Ala Gln Ala Arg Ala Gly Gly Gly Arg Arg Tyr Gln Ser Thr Val
145                 150                 155                 160

Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp
                165                 170                 175

Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala
            180                 185                 190

Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn
        195                 200                 205

Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala
    210                 215                 220

Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr
225                 230                 235                 240
```

```
Arg His Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys
                245                 250                 255

Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly
            260                 265                 270

Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe
        275                 280                 285

Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Ala Ala Cys Thr Ser
    290                 295                 300

Arg Glu Ala Pro Phe
305
```

<210> 9
<211> 312
<212> PRT
<213> Homo sapiens

<400> 9

```
Met Val Gly Leu Lys Pro Ser Asp Val Pro Pro Thr Met Ala Val Lys
  1               5                  10                  15

Phe Leu Gly Ala Gly Thr Ala Ala Cys Phe Ala Asp Leu Val Thr Phe
             20                  25                  30

Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Asn Gln
         35                  40                  45

Ala Val Gln Thr Ala Arg Leu Val Gln Tyr Arg Gly Val Leu Gly Thr
     50                  55                  60

Ile Leu Thr Met Val Arg Thr Glu Gly Pro Cys Ser Pro Tyr Asn Gly
 65                  70                  75                  80

Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Ile Arg Ile
                 85                  90                  95

Gly Leu Tyr Asp Ser Val Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp
            100                 105                 110

Asn Ser Ser Leu Thr Thr Arg Ile Leu Ala Gly Cys Thr Thr Gly Ala
        115                 120                 125

Met Ala Val Thr Cys Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
    130                 135                 140

Gln Ala Ser Ile His Leu Gly Pro Ser Arg Ser Asp Arg Lys Tyr Ser
145                 150                 155                 160

Gly Thr Met Asp Ala Tyr Arg Thr Ile Ala Arg Glu Glu Gly Val Arg
                165                 170                 175

Gly Leu Trp Lys Gly Thr Leu Pro Asn Ile Met Arg Asn Ala Ile Val
            180                 185                 190
```

Asn Cys Ala Glu Val Val Thr Tyr Asp Ile Leu Lys Glu Lys Leu Leu
195 200 205

Asp Tyr His Leu Leu Thr Asp Asn Phe Pro Cys His Phe Val Ser Ala
210 215 220

Phe Gly Ala Gly Phe Cys Ala Thr Val Val Ala Ser Pro Val Asp Val
225 230 235 240

Val Lys Thr Arg His Met Asn Ser Pro Pro Gly Gln Tyr Phe Ser Pro
245 250 255

Leu Asp Cys Met Ile Lys Met Val Ala Gln Glu Gly Pro Thr Ala Phe
260 265 270

Tyr Lys Gly Phe Thr Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val
275 280 285

Val Met Phe Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Lys Val
290 295 300

Gln Met Leu Arg Glu Ser Pro Phe
305 310

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA Primer

<400> 10
ttttttttttt ttttttttttt tttt 24

<210> 11
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved UCP Peptide Fragment

<400> 11
Cys Cys Ile Tyr Thr Ile Gly Ala Tyr Ala Cys Ile Gly Cys Ile Ala
1 5 10 15

Ala Arg

<210> 12
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved UCP Peptide Fragment

<400> 12
Ala Cys Trp Thr Thr Cys Cys Ala Ile Ser Tyr Ile Cys Cys Ile Ala
1 5 10 15

Trp Ile Cys